

# SEQUENCE LISTING

<110> Duprat, Fabrice  
Lesage, Florian  
Fink, Michel  
Lazdunski, Michel

<120> FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING  
AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS

<130> 1201-CIP-DIV-2-00

<141> 2001-08-24

<150> 09/144,914

<151> 1998-09-01

<150> 08/749,816

<151> 1996-11-15

<150> 60/095,234

<151> 1998-08-04

<150> FR 96/01565

<151> 1996-02-08

<160> 24

<170> PatentIn Ver. 2.0

<210> 1

<211> 1894

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (183)..(1190)

<220>

<223> TWIK-1

<400> 1

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cgcgctccgg ccggtctgcg gcgttggcct tggctttggc tttggcgggc gcggtggaga 180
ag atg ctg cag tcc ctg gcc ggc agc tcg tgc gtg cgc ctg gtg gag 227
Met Leu Gln Ser Leu Ala Gly Ser Ser Cys Val Arg Leu Val Glu
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Arg His Arg Ser Ala Trp Cys Phe Gly Phe Leu Val Leu Gly Tyr Leu
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ctc tac ctg gtc ttc ggc gca gtg gtc ttc tcc tcg gtg gag ctg ccc 323
Leu Tyr Leu Val Phe Gly Ala Val Val Phe Ser Ser Val Glu Leu Pro
35 40 45

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tat gag gac ctg ctg cgc cag gag ctg cgc aag ctg aag cga cgc ttc 371  
Tyr Glu Asp Leu Leu Arg Gln Glu Leu Arg Lys Leu Lys Arg Arg Phe  
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ttg gag gag cac gag tgc ctg tct gag cag cag ctg gag cag ttc ctg 419  
Leu Glu Glu His Glu Cys Leu Ser Glu Gln Gln Leu Glu Gln Phe Leu  
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100 105 110

agc acc gtg ctc tcc acc aca ggt tat ggc cac acc gtg ccc ttg tca 563  
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Phe Thr Leu Leu Phe Leu Thr Ala Val Val Gln Arg Ile Thr Val His  
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180 185 190

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Val Ser Cys Phe Phe Phe Ile Pro Ala Ala Val Phe Ser Val Leu Glu  
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gat gac tgg aac ttc ctg gaa tcc ttt tat ttt tgt ttt att tcc ctg 851  
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210 215 220

agc acc att ggc ctg ggg gat tat gtg cct ggg gaa ggc tac aat caa 899  
Ser Thr Ile Gly Leu Gly Asp Tyr Val Pro Gly Glu Gly Tyr Asn Gln  
225 230 235

aaa ttc aga gag ctc tat aag att ggg atc acg tgt tac ctg cta ctt 947  
Lys Phe Arg Glu Leu Tyr Lys Ile Gly Ile Thr Cys Tyr Leu Leu Leu  
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ggc ctt att gcc atg ttg gta gtt ctg gaa acc ttc tgt gaa ctc cat 995  
Gly Leu Ile Ala Met Leu Val Val Leu Glu Thr Phe Cys Glu Leu His  
260 265 270

gag ctg aaa aaa ttc aga aaa atg ttc tat gtg aag aag gac aag gac 1043  
Glu Leu Lys Lys Phe Arg Lys Met Phe Tyr Val Lys Lys Asp Lys Asp  
275 280 285

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TC44280-284550

Glu Asp Gln Val His Ile Ile Glu His Asp Gln Leu Ser Phe Ser Ser  
 290 295 300

atc aca gac cag gca gct ggc atg aaa gag gac cag aag caa aat gag 1139  
 Ile Thr Asp Gln Ala Ala Gly Met Lys Glu Asp Gln Lys Gln Asn Glu  
 305 310 315

cct ttt gtg gcc acc cag tca tct gcc tgc gtg gat ggc cct gca aac 1187  
 Pro Phe Val Ala Thr Gln Ser Ser Ala Cys Val Asp Gly Pro Ala Asn  
 320 325 330 335

cat tgagcgtagg atttggtgca ttatgctaga gcaccagggt cagggtgcaa 1240  
 His

ggaagaggct taagtatggt catttttatc agaatgcaaa agcgaaaatt atgtcacttt 1300

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<213> Homo sapiens

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Tyr Leu Val Phe Gly Ala Val Val Phe Ser Ser Val Glu Leu Pro Tyr  
 35 40 45

Glu Asp Leu Leu Arg Gln Glu Leu Arg Lys Leu Lys Arg Arg Phe Leu  
 50 55 60

Glu Glu His Glu Cys Leu Ser Glu Gln Gln Leu Glu Gln Phe Leu Gly  
 65 70 75 80

Arg Val Leu Glu Ala Ser Asn Tyr Gly Val Ser Val Leu Ser Asn Ala  
 85 90 95  
 Ser Gly Asn Trp Asn Trp Asp Phe Thr Ser Ala Leu Phe Phe Ala Ser  
 100 105 110  
 Thr Val Leu Ser Thr Thr Gly Tyr Gly His Thr Val Pro Leu Ser Asp  
 115 120 125  
 Gly Gly Lys Ala Phe Cys Ile Ile Tyr Ser Val Ile Gly Ile Pro Phe  
 130 135 140  
 Thr Leu Leu Phe Leu Thr Ala Val Val Gln Arg Ile Thr Val His Val  
 145 150 155 160  
 Thr Arg Arg Pro Val Leu Tyr Phe His Ile Arg Trp Gly Phe Ser Lys  
 165 170 175  
 Gln Val Val Ala Ile Val His Ala Val Leu Leu Gly Phe Val Thr Val  
 180 185 190  
 Ser Cys Phe Phe Phe Ile Pro Ala Ala Val Phe Ser Val Leu Glu Asp  
 195 200 205  
 Asp Trp Asn Phe Leu Glu Ser Phe Tyr Phe Cys Phe Ile Ser Leu Ser  
 210 215 220  
 Thr Ile Gly Leu Gly Asp Tyr Val Pro Gly Glu Gly Tyr Asn Gln Lys  
 225 230 235 240  
 Phe Arg Glu Leu Tyr Lys Ile Gly Ile Thr Cys Tyr Leu Leu Leu Gly  
 245 250 255  
 Leu Ile Ala Met Leu Val Val Leu Glu Thr Phe Cys Glu Leu His Glu  
 260 265 270  
 Leu Lys Lys Phe Arg Lys Met Phe Tyr Val Lys Lys Asp Lys Asp Glu  
 275 280 285  
 Asp Gln Val His Ile Ile Glu His Asp Gln Leu Ser Phe Ser Ser Ile  
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 <222> (126)..(1307)

<220>  
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 Val Thr Thr Leu Ala Leu Ile Val Cys Thr

ttc acc tac ctg ctg gtg ggc gcc gcg gtc ttc gac gcg ctg gag tcg 218  
Phe Thr Tyr Leu Leu Val Gly Ala Ala Val Phe Asp Ala Leu Glu Ser  
20 25 30

gag ccc gag ctg atc gag cgg cag cgg ctg gag ctg cgg cag cag gag 266  
Glu Pro Glu Leu Ile Glu Arg Gln Arg Leu Glu Leu Arg Gln Gln Glu  
35 40 45

ctg cgg gcg cgc tac aac ctc agc cag ggc ggc tac gag gag ctg gag 314  
Leu Arg Ala Arg Tyr Asn Leu Ser Gln Gly Gly Tyr Glu Glu Leu Glu  
50 55 60

cgc gtc gtg ctg cgc ctc aag ccg cac aag gcc ggc gtg cag tgg cgc 362  
Arg Val Val Leu Arg Leu Lys Pro His Lys Ala Gly Val Gln Trp Arg  
65 70 75

ttc gcc ggc tcc ttc tac ttc gcc atc acc gtc atc acc acc atc ggc 410  
Phe Ala Gly Ser Phe Tyr Phe Ala Ile Thr Val Ile Thr Thr Ile Gly  
80 85 90 95

tac ggg cac gcg gca ccc agc acg gat ggc ggc aag gtg ttc tgc atg 458  
 Tyr Gly His Ala Ala Pro Ser Thr Asp Gly Gly Lys Val Phe Cys Met  
 100 105 110

ttc tac gcg ctg ctg ggc atc ccg ctc acg ctc gtc atg ttc cag agc 506  
Phe Tyr Ala Leu Leu Gly Ile Pro Leu Thr Leu Val Met Phe Gln Ser  
115 120 125

ctg ggc gag cgc atc aac acc ttg gtg agg tac ctg ctg cac cgc gcc 554  
Leu Gly Glu Arg Ile Asn Thr Leu Val Arg Tyr Leu Leu His Arg Ala  
130 135 140

aag aag ggg ctg ggc atg cgg cgc gcc gac gtg tcc atg gcc aac atg 602  
Lys Lys Gly Leu Gly Met Arg Arg Ala Asp Val Ser Met Ala Asn Met  
145 150 155

gtg ctc atc ggc ttc ttc tcg tgc atc agc acg ctg tgc atc ggc gcc 650  
Val Leu Ile Gly Phe Phe Ser Cys Ile Ser Thr Leu Cys Ile Gly Ala  
160 165 170 175

gcc gcc ttc tcc cac tac gag cac tgg acc ttc ttc cag gcc tac tac 698  
Ala Ala Phe Ser His Tyr Glu His Trp Thr Phe Phe Gln Ala Tyr Tyr  
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tac	tgc	ttc	atc	acc	ctc	acc	acc	atc	ggc	ttc	ggc	gac	tac	gtg	gcg	746
Tyr	Cys	Phe	Ile	Thr	Leu	Thr	Thr	Ile	Gly	Phe	Gly	Asp	Tyr	Val	Ala	
			195					200					205			

ctg cag aag gac cag gcc ctg cag acg cag ccg cag tac gtg gcc ttc 794  
Leu Gln Lys Asp Gln Ala Leu Gln Thr Gln Pro Gln Tyr Val Ala Phe  
210 215 220



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 <213> Homo sapiens

<220>  
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 Pro Glu Leu Ile Glu Arg Gln Arg Leu Glu Leu Arg Gln Gln Glu Leu  
 35 40 45  
 Arg Ala Arg Tyr Asn Leu Ser Gln Gly Gly Tyr Glu Glu Leu Glu Arg  
 50 55 60  
 Val Val Leu Arg Leu Lys Pro His Lys Ala Gly Val Gln Trp Arg Phe  
 65 70 75 80  
 Ala Gly Ser Phe Tyr Phe Ala Ile Thr Val Ile Thr Thr Ile Gly Tyr  
 85 90 95  
 Gly His Ala Ala Pro Ser Thr Asp Gly Gly Lys Val Phe Cys Met Phe  
 100 105 110  
 Tyr Ala Leu Leu Gly Ile Pro Leu Thr Leu Val Met Phe Gln Ser Leu  
 115 120 125  
 Gly Glu Arg Ile Asn Thr Leu Val Arg Tyr Leu Leu His Arg Ala Lys  
 130 135 140  
 Lys Gly Leu Gly Met Arg Arg Ala Asp Val Ser Met Ala Asn Met Val

145		150		155		160									
Leu	Ile	Gly	Phe	Phe	Ser	Cys	Ile	Ser	Thr	Leu	Cys	Ile	Gly	Ala	Ala
				165					170					175	
Ala	Phe	Ser	His	Tyr	Glu	His	Trp	Thr	Phe	Phe	Gln	Ala	Tyr	Tyr	Tyr
			180					185					190		
Cys	Phe	Ile	Thr	Leu	Thr	Thr	Ile	Gly	Phe	Gly	Asp	Tyr	Val	Ala	Leu
		195					200					205			
Gln	Lys	Asp	Gln	Ala	Leu	Gln	Thr	Gln	Pro	Gln	Tyr	Val	Ala	Phe	Ser
	210					215					220				
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225					230					235					240
Leu	Val	Val	Leu	Arg	Phe	Met	Thr	Met	Asn	Ala	Glu	Asp	Glu	Lys	Arg
				245					250					255	
Asp	Ala	Glu	His	Arg	Ala	Leu	Leu	Thr	Arg	Asn	Gly	Gln	Ala	Gly	Gly
			260					265					270		
Gly	Gly	Gly	Gly	Gly	Ser	Ala	His	Thr	Thr	Asp	Thr	Ala	Ser	Ser	Thr
		275					280					285			
Ala	Ala	Ala	Gly	Gly	Gly	Gly	Phe	Arg	Asn	Val	Tyr	Ala	Glu	Val	Leu
	290					295					300				
His	Phe	Gln	Ser	Met	Cys	Ser	Cys	Leu	Trp	Tyr	Lys	Ser	Arg	Glu	Lys
305					310					315					320
Leu	Gln	Tyr	Ser	Ile	Pro	Met	Ile	Ile	Pro	Arg	Asp	Leu	Ser	Thr	Ser
				325					330					335	
Asp	Thr	Cys	Val	Glu	Gln	Ser	His	Ser	Ser	Pro	Gly	Gly	Gly	Gly	Arg
			340					345					350		
Tyr	Ser	Asp	Thr	Pro	Ser	Arg	Arg	Cys	Leu	Cys	Ser	Gly	Ala	Pro	Arg
		355					360					365			
Ser	Ala	Ile	Ser	Ser	Val	Ser	Thr	Gly	Leu	His	Ser	Leu	Ser	Thr	Phe
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 <212> PRT  
 <213> Murine

<220>  
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Pro Met Ile Ile Pro Arg Asp Leu Ser Thr Ser Asp Thr Cys Val Glu  
340 345 350





Ile Pro Lys Asp Met Trp Thr Phe Ser Ser Ala Leu Val Phe Thr Thr  
 130 135 140  
 Thr Thr Val Ile Pro Val Gly Tyr Gly Tyr Ile Phe Pro Val Ser Ala  
 145 150 155 160  
 Tyr Gly Arg Met Cys Leu Ile Ala Tyr Ala Leu Leu Gly Ile Pro Leu  
 165 170 175  
 Thr Leu Val Thr Met Ala Asp Thr Gly Lys Phe Ala Ala Gln Leu Val  
 180 185 190  
 Thr Arg Trp Phe Gly Asp Asn Asn Met Ala Ile Pro Ala Ala Ile Phe  
 195 200 205  
 Val Cys Leu Leu Phe Ala Tyr Pro Leu Val Val Gly Phe Ile Leu Cys  
 210 215 220  
 Ser Thr Ser Asn Ile Thr Tyr Leu Asp Ser Val Tyr Phe Ser Leu Thr  
 225 230 235 240  
 Ser Ile Phe Thr Ile Gly Phe Gly Asp Leu Thr Pro Asp Met Asn Val  
 245 250 255  
 Ile His Met Val Leu Phe Leu Ala Val Gly Val Ile Leu Val Thr Ile  
 260 265 270  
 Thr Leu Asp Ile Val Ala Ala Glu Met Ile Asp Arg Val His Tyr Met  
 275 280 285  
 Gly Arg His Val Gly Lys Ala Lys Glu Leu Ala Gly Lys Met Phe Gln  
 290 295 300  
 Leu Ala Gln Ser Leu Asn Met Lys Gln Gly Leu Val Ser Gly Val Gly  
 305 310 315 320  
 Gln Leu His Ala Leu Ala Arg Phe Gly Met Leu Val Gly Arg Glu Glu  
 325 330 335  
 Val Asp Lys Thr Gln Glu Asp Gly Ile Ile Ala Phe Ser Pro Asp Val  
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 Ser Arg Arg Ser Ala Glu Asn Ser Ala Arg Asn Leu Phe Leu Ser  
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<220>  
 <223> TREK-1

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Thr	Ile	Phe	Leu	Val	Val	Val	Leu	Tyr	Leu	Ile	Ile	Gly	Ala	Ala	Val
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Val	Ile	Gln	Lys	Gln	Thr	Phe	Ile	Ala	Gln	His	Ala	Cys	Val	Asn	Ser
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Thr	Glu	Leu	Asp	Glu	Leu	Ile	Gln	Gln	Ile	Val	Ala	Ala	Ile	Asn	Ala
			100					105					110		
Gly	Ile	Ile	Pro	Leu	Gly	Asn	Ser	Ser	Asn	Gln	Val	Ser	His	Trp	Asp
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Ile	Tyr	Ala	Leu	Leu	Gly	Ile	Pro	Leu	Glu	Gly	Phe	Leu	Leu	Ala	Gly
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Val	Gly	Asp	Gln	Leu	Gly	Thr	Ile	Phe	Gly	Lys	Gly	Ile	Ala	Lys	Val
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Glu	Asp	Thr	Phe	Ile	Lys	Trp	Asn	Val	Ser	Gln	Thr	Lys	Ile	Arg	Ile
		195					200					205			
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	210					215					220				
Leu	Pro	Ala	Val	Ile	Phe	Lys	His	Ile	Glu	Gly	Trp	Ser	Ala	Leu	Asp
225					230					235					240
Ala	Ile	Tyr	Phe	Val	Val	Ile	Thr	Leu	Thr	Thr	Ile	Gly	Phe	Gly	Asp
				245					250					255	
Tyr	Val	Ala	Gly	Gly	Ser	Asp	Ile	Glu	Tyr	Leu	Asp	Phe	Tyr	Lys	Pro
			260					265					270		
Val	Val	Trp	Phe	Trp	Ile	Leu	Val	Gly	Leu	Ala	Tyr	Phe	Ala	Ala	Val
		275					280					285			
Leu	Ser	Met	Ile	Gly	Asp	Trp	Leu	Arg	Val	Ile	Ser	Lys	Lys	Thr	Lys
	290					295					300				
Glu	Glu	Val	Gly	Glu	Phe	Arg	Ala	His	Ala	Ala	Glu	Trp	Thr	Ala	Asp
305					310					315					320
Val	Thr	Ala	Glu	Phe	Lys	Glu	Thr	Arg	Arg	Arg	Leu	Ser	Val	Glu	Ile
				325					330					335	

Tyr Asp Lys Phe Gln Arg Ala Thr Ser Val Lys Arg Lys Leu Ser Ala  
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Cys Leu  
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<212> PRT  
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<220>  
<223> TWIK-1 P1

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Tyr Gly His Thr Val Pro Leu Ser Asp Gly Gly  
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<210> 10  
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<212> PRT  
<213> Homo sapiens

<220>  
<223> TWIK-1 P2

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Leu Gly Asp Tyr Val Pro Gly Glu Gly Tyr Asn  
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<220>  
<223> Description of Unknown Organism: P domain of  
representative K<sup>+</sup> channel sequence

<220>  
<223> TOK-1 P2

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Tyr Gly Asp Tyr Ala Pro Arg Thr Gly Ala Gly  
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<213> Unknown
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representative K+ channel sequence
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Leu Gly Asp Ile Leu Pro Lys Ser Val Gly Ala
                20                      25
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<220>  
<223> Slo

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Tyr Gly Asp Val Tyr Cys Glu Thr Val Leu Gly
          20                      25

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<210>	14
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<220>  
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Tyr Gly Asp Met Thr Pro Val Gly Phe Trp Gly
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Tyr Gly Asp Met Thr Pro Val Gly Phe Trp Gly  
20 25

<210>	15
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<220>  
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<210>	16
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<212>	PRT
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<220>  
<223> Description of Unknown Organism: P domain of representative K<sup>+</sup> channel sequence

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<223> Sha1

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<400> 16
Ile Pro Ala Ala Phe Trp Tyr Thr Ile Val Thr Met Thr Thr Leu Gly
  1               5               10               15

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Tyr Gly Asp Met Val Pro Glu Thr Ile Ala Gly  
20 25

<210>	17
<211>	27
<212>	PRT
<213>	Unknown

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<220>
<223> Description of Unknown Organism: P domain of
representative K+ channel sequence
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<220>  
<223> Shaw

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<400> 17
Ile Pro Leu Gly Leu Trp Trp Ala Leu Val Thr Met Thr Thr Val Gly
  1             5             10             15
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Tyr Gly Asp Met Ala Pro Lys Thr Tyr Ile Gly  
20 25

<210> 18

<211> 27  
<212> PRT  
<213> Unknown

<220>  
<223> Description of Unknown Organism: P domain of  
representative K+ channel sequence

<220>  
<223> KAT1

<400> 18  
Tyr Val Thr Ala Leu Tyr Trp Ser Ile Thr Thr Leu Thr Thr Gly  
1 5 10 15

Tyr Gly Asp Phe His Ala Glu Asn Pro Arg Glu  
20 25

<210> 19  
<211> 27  
<212> PRT  
<213> Unknown

<220>  
<223> Description of Unknown Organism: P domain of  
representative K+ channel sequence

<220>  
<223> AKT1

<400> 19  
Tyr Val Thr Ser Met Tyr Trp Ser Ile Thr Thr Leu Thr Thr Val Gly  
1 5 10 15

Tyr Gly Asp Ile His Pro Val Asn Thr Lys Glu  
20 25

<210> 20  
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<212> PRT  
<213> Unknown

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representative K+ channel sequence

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Phe Gly Asn Val Ala Ala Glu Thr Asp Asn Glu  
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<210> 21  
<211> 27

<212> PRT  
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<220>  
<223> Description of Unknown Organism: P domain of  
representative K+ channel sequence

<220>  
<223> ROMK1

<400> 21  
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1 5 10 15

Tyr Gly Phe Arg Phe Val Thr Glu Gln Cys Ala  
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<210> 22  
<211> 27  
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<213> Unknown

<220>  
<223> Description of Unknown Organism: P domain of  
representative K+ channel sequence

<220>  
<223> IRK1

<400> 22  
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1 5 10 15

Tyr Gly Phe Arg Cys Val Thr Asp Glu Cys Pro  
20 25

<210> 23  
<211> 27  
<212> PRT  
<213> Unknown

<220>  
<223> Description of Unknown Organism: P domain of  
representative K+ channel sequence

<220>  
<223> GIRK1

<400> 23  
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1 5 10 15

Tyr Gly Tyr Arg Tyr Ile Thr Asp Lys Cys Pro  
20 25

<210> 24  
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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: antisense  
oligonucleotide complementary to the partial  
mouse cDNA sequence of TASK

<400> 24

caccagcagg taggtgaagg tgcacacgat gagagccaac gtgcgcac

48

093343-0340  
T04280-0340